

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 18:23:55 ; Search time 2186.19 Seconds
(without alignments)
16364.623 Million cell updates/sec

Title: US-10-026-106E-9

Perfect score: 1772
Sequence: 1 aagggccatgscgggcccga.....acatccaccgaatcgtatg 1472

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

| | |
|-----|--------------|
| 1: | em_estda:* |
| 2: | em_esthm:* |
| 3: | em_estin:* |
| 4: | em_estnu:* |
| 5: | em_estov:* |
| 6: | em_estpl:* |
| 7: | em_estro:* |
| 8: | em_estc:* |
| 9: | gb_estc:* |
| 10: | gb_estc2:* |
| 11: | gb_estc3:* |
| 12: | gb_estc4:* |
| 13: | gb_estc5:* |
| 14: | gb_estc6:* |
| 15: | em_estfun:* |
| 16: | em_estcom:* |
| 17: | em_gse_hum:* |
| 18: | em_gse_inv:* |
| 19: | em_gse_pln:* |
| 20: | em_gse_vrt:* |
| 21: | em_gse_fun:* |
| 22: | em_gse_mam:* |
| 23: | em_gse_mus:* |
| 24: | em_gse_pro:* |
| 25: | em_gse_rod:* |
| 26: | em_gse_phg:* |
| 27: | em_gse_vrt:* |
| 28: | gb_gse1:* |
| 29: | gb_gse2:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1 | 598.8 | 40.7 | 1078 | 12 | B0061188 |
| 2 | 477.6 | 32.4 | 508 | 10 | BR244935 |
| 3 | 375.4 | 25.5 | 430 | 10 | BR246345 |
| 4 | 372 | 25.3 | 836 | 13 | BUI51377 |

| | | | | | |
|----|-------|------|------|----|----------|
| 5 | 370.4 | 25.2 | 991 | 12 | B0056204 |
| 6 | 355.6 | 24.2 | 476 | 28 | AQ610898 |
| 7 | 350.2 | 23.8 | 358 | 13 | B0430530 |
| 8 | 348.4 | 23.7 | 964 | 13 | BQ894374 |
| 9 | 341 | 23.2 | 640 | 14 | BY729118 |
| 10 | 335 | 22.8 | 541 | 28 | AQ610868 |
| 11 | 292 | 19.8 | 558 | 28 | AQ645533 |
| 12 | 237.4 | 16.1 | 620 | 12 | BT104593 |
| 13 | 223.8 | 15.2 | 496 | 14 | CB713061 |
| 14 | 193.8 | 13.2 | 609 | 14 | CB713061 |
| 15 | 188.2 | 12.8 | 606 | 28 | BI657868 |
| 16 | 134.8 | 9.2 | 506 | 28 | AQ772013 |
| 17 | 134.4 | 9.1 | 555 | 14 | CB738101 |
| 18 | 89 | 6.0 | 392 | 13 | BY093564 |
| 19 | 56.6 | 3.8 | 800 | 13 | B0237675 |
| 20 | 55.2 | 3.8 | 663 | 12 | BT043372 |
| 21 | 50.2 | 3.4 | 925 | 29 | CNS0091P |
| 22 | 47.2 | 3.2 | 391 | 14 | CB775730 |
| 23 | 47.2 | 3.2 | 1201 | 13 | BX381961 |
| 24 | 46.2 | 3.1 | 704 | 10 | BG747302 |
| 25 | 44.8 | 3.0 | 485 | 13 | BQ374676 |
| 26 | 43.8 | 3.0 | 341 | 29 | B2367545 |
| 27 | 43.4 | 2.9 | 280 | 12 | BI063605 |
| 28 | 43 | 2.9 | 709 | 28 | B2121065 |
| 29 | 43 | 2.9 | 914 | 9 | AL524362 |
| 30 | 42.4 | 2.9 | 967 | 12 | BT108915 |
| 31 | 42.4 | 2.9 | 1020 | 13 | BQ073607 |
| 32 | 42 | 2.9 | 878 | 13 | B0911485 |
| 33 | 41.8 | 2.8 | 499 | 12 | BJ059876 |
| 34 | 41.6 | 2.8 | 680 | 9 | AV834441 |
| 35 | 41.6 | 2.8 | 931 | 29 | CNS06SAL |
| 36 | 41.4 | 2.8 | 682 | 28 | AZ793096 |
| 37 | 41.2 | 2.8 | 334 | 13 | BY103116 |
| 38 | 41.2 | 2.8 | 406 | 9 | AV392658 |
| 39 | 41.2 | 2.8 | 450 | 9 | AV392658 |
| 40 | 41.2 | 2.8 | 488 | 9 | AV635124 |
| 41 | 41.2 | 2.8 | 504 | 9 | AV388620 |
| 42 | 41.2 | 2.8 | 509 | 9 | AV636333 |
| 43 | 41.2 | 2.8 | 519 | 9 | AV390975 |
| 44 | 41.2 | 2.8 | 524 | 9 | AV620459 |
| 45 | 41.2 | 2.8 | 550 | 9 | AV392161 |

ALIGNMENTS

RESULT 1
LOCUS B0061188 1078 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6863006 NIH_MGC_99 Homo sapiens cDNA clone IMAGE15920208
ACCESSION B0061188
VERSION B0061188.1 GI:19884982
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strusberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLC2083 row: 1 column: 09
High quality sequence stop: 593.

FEATURES
Location/Qualifiers
1. 1078
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5920208"
/clone_lib="NIH_MGC_99"
/lab_host="DH10B (phage-resistant)"
/clone="Organism: lymph; Vector: pOT8; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 243 a 306 c 309 g 219 t 1 others

Query Match 40.7%; Score 598.8; DB 12; Length 1078;
Best Local Similarity 96.1%; Pred. No. 4.6e-126;
Matches 624; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

16 CCCGAGCGCTGGGGCCCCCTGCTCTGCTGCTGCAAGCCCTCCAG--GGAGCCCC 73
108 CCCGAGAGCAAGCACTGAGCTCTGGGGCCCTGCGCTCCCGGAGAGAGAGAGCCCC 167
74 GTCTGGCCCCCTCCCAAGATGATGACCTCTCTCCCAAGATTCAGCGTACCTGACAT 133
168 GTCTGGCCCCCTCCCAAGATGATGACCTCTCTCCCAAGATTCAGCGTACCTGACAT 227
134 GCGTCCGAGCGCTGGAGAACCCCAAGATGATGATTTGTTGCTTACAGCTCTC 193
228 GCGTCCGAGCGCTGGAGAACCCCAAGATGATGATTTGTTGCTTACAGCTCTC 287
194 CCACCGGTAGACGGTGGCGGAGTGGAGTGGCGGAGCCAGAGACTCTATGTT 253
288 CCACCGGTAGACGGTGGCGGAGTGGAGTGGCGGAGCCAGAGACTCTATGTT 347
254 CATGATGTGCTGAGAGAACAGAGCTGTACAAAGTTGAGAGAGCGGTGGAGCG 313
348 CATGATGTGCTGAGAGAACAGAGCTGTACAAAGTTGAGAGAGCGGTGGAGCG 407
314 TTTCTCCAGCTCCAGATCTCCCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 373
408 TTTCTCCAGCTCCAGATCTCCCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 467
374 TGGAGCGGGCGGAGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
468 TGGAGCGGGCGGAGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
434 CCAAGTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
528 CCAAGTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
494 GGAAGAGAGGGGGCGGAGAACAGAGCTATTTTCAGTCACTCCCATGCGCAGCG 553
588 GGAAGAGAGGGGGCGGAGAACAGAGCTATTTTCAGTCACTCCCATGCGCAGCG 647
554 AGATCACTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
648 AGATCACTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
614 CGTTCAAGTCTCCGAAAATAGAGCAAGTCTCTTAAGCCCACTGCTTCTT 662
708 CGTTCAAGTCTCCGAAAATAGAGCAAGTCTCTTAAGCCCACTGCTTCTT 756

RESULT 2
BE244935 508 bp mRNA linear EST 03-OCT-2001
LOCUS

DEFINITION
TCBAP2669 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project:TCBA Homo sapiens cDNA clone TCBAP2669, mRNA
sequence.

ACCESSION
BR244935

VERSION
BR244935.1 GI:9096765

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 508)
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
Bouck, J., Gbabe, R.A. and Margolin, J.F.
Pediatric Leukemia cDNA Sequencing Project

TITLE
JOURNAL

COMMENT
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer

FEATURES
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP2669"
/sex="male"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project:TCBA"
/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'-GGAGAGCTCAGCGCGCCGAGAGAGCT(VN
3')-V-A-C-G; N-A-C-G/T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'-AGAGAGCTCGATCCGCGCGCCGAGAGAGCTTGAAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,
Itoh M., Nagaoka S., Sasaki, K., Okazaki Y., Muramatsu M.,
Schneider C., Hayashizaki Y. High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)."

BASE COUNT 108 a 147 c 160 g 93 t

Query Match 32.4%; Score 477.6; DB 10; Length 508;
Best Local Similarity 98.4%; Pred. No. 1.6e-98;
Matches 504; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

798 TCGAGGCGCCGAGCCCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857
1 TCGAGGCGCCGAGCCCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
858 AGAGAGATGAG 917
61 AGAGAGATGAG 119
918 CTTTCCGAGGAG 977
120 CTTTCCGAGGAG 116
978 CAGGAGAGCCGAGGAGCTCTGCTGCTCCAGAGAGAGCTCTGCTGCTGAGATTCTTCA 1037

Db 177 CAGGAGAGCCCAAGGCTCTCTGCTGCTCCAGAGAGGCTCTCTGCTTGGATTCTTGA 236

Qy 1038 ACAGAACTGGGCGACGACTGTGAGACTCTCTCTGGGACAGAGGCTCTCTGCTTAT 1097

Db 237 ACAGAACTGGGCGACGACTGTGAGACTCTCTCTGGGACAGAGGCTCTCTGCTTAT 296

Qy 1098 TGGCTGAGAGAGGCGACGAGGCTGGGAGTGGGAGTGGGACCAAGATCTCTCCAC 1157

Db 297 TGGCTGAGAGAGGCGACGAGGCTGGGAGTGGGAGTGGGACCAAGATCTCTCCAC 356

Qy 1158 CACCTGAATCTCCAGAGACTGGGTTTCTGTGAGAGGCTCCAGAGATTAACCTCTCT 1217

Db 357 CACCTGAATCTCCAGAGACTGGGTTTCTGTGAGAGGCTCCAGAGATTAACCTCTCTCT 416

Qy 1218 CCTGGGCACTGGGCGACCTTACCAAGGAGGAGATCTGTCTCTGGGAGACCCGAG 1277

Db 417 CTTGGGCACTGGGCGACCTTACCAAGGAGGAGATCTGTCTCTGGGAGACCCGAG 476

Qy 1278 TTTCTCTTCCAGACCTGACCTTCTGCTGGAA 1309

Db 477 TTTCTCTTCCAGACCTGACCTTCTGCTGGAA 508

RESULT 3
LOCUS BE246345
DEFINITION 430 bp mRNA linear EST 03-OCT-2001
TCEAP1D2918 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HSC project-TCEA Homo sapiens cDNA clone TCEAP2918, mRNA
sequence.
ACCESSION BE246345
VERSION BE246345.1 GI:9098094
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 430)
Weil, Y., Tsang, Y.T.W., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric Leukemia cDNA Sequencing Project
unpublished
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Clatation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
Location/Qualifiers
1. 430
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCEAP2918"
/sex="male"
/tissue_type="leukophoresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HSC project-TCEA"
/note="Vector: lambda pBS; Site 1: BamHI; Site 2: EcoRI;
first strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'-GAGAGACTCGAGCGCGCAGAGAG(7)VN
3'-VA-C/G; NA-C/G, T) and then digested with BamHI and XhoI.
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of

Query Match 25.5%; Score 375.4; DB 10; Length 430;
Best Local Similarity 96.3%; Pred. No. 3.2e-75;
Matches 417; Conservative 0; Mismatches 11; Indels 5; Gaps 3;
BASE COUNT 95 a 120 c 136 g 79 t
ORIGIN
1ambda pSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997).
Qy 798 TCAGGAGGCGGCGACGAGGCTGAGTGAAGAGGAGGCTTGCAGAGGAGGAGG 857
Db 1 TCAGGAGGCGGCGACGAGGCTGAGTGAAGAGGAGGCTTGCAGAGGAGGAGG 60
Qy 858 AGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 917
Db 61 AGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 918 CTTTCTGGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 977
Db 121 CTTTCTGGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1177
Qy 978 CAGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1037
Db 178 CAGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 237
Qy 1038 ACAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1097
Db 238 ACAGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 297
Qy 1098 TGGCTGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1157
Db 298 TGGCTGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Qy 1158 CACCTGAATCTCCAGAGACTGGGCTTCTGTGAGAGGCTCCAGAGATTAACCTCTC 1215
Db 358 CACCTGAATCTCCAGAGACTGGGATTTCTGTGAGAGGCTCCAGAGATTAACCTCTC 417
Qy 1216 CTCCTGGGCGGAGG 1228
Db 418 CTCCTGGGCGGAGG 430
RESULT 4
LOCUS BU151377/c 836 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT 8585742 NIH_MGC_99 Homo sapiens cDNA clone IMAGR:6304649
5', mRNA sequence.
ACCESSION BU151377
VERSION BU151377.1 GI:22664909
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 836)
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
plate: LMC2525 row: k column: 18

FEATURES
source

High quality sequence stop: 522.
Location/Qualifiers

1. 836
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:6304649"
/issue="IMB:6304649"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 185 a 223 c 240 g 186 t 2 others
ORIGIN

Query Match 25.3%; Score 372; DB 13; Length 836;
Best Local Similarity 99.2%; Pred. No. 2.4e-74;
Matches 385; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

674 CAGGACTTTTCTGACACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 733
541 CAGGACTTTTCTGACACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 482
734 GTGAATGACTTGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
481 GTGAATGACTTGTCT 422
794 CAGGACTTTTCTGACACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 853
421 CAGGACTTTTCTGACACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 362
854 GAGGAGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 913
361 GAGGAGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
914 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
301 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245
974 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
244 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
1034 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 1061
184 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 157

RESULT 5
B0056204/c 991 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT 6773374 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808505
DEFINITION 5' mRNA sequence.
ACCESSION B0056204
VERSION B0056204.1 GI:19815544
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 991)
NIH-MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgaaba@mail.nih.gov

FEATURES
source

Tissue Procurement: Lou Straub
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LHC2052 row: k column: 02
High quality sequence stop: 645.
Location/Qualifiers

1. 991
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:5808505"
/issue="IMB:5808505"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 224 a 285 c 270 g 211 t 1 others
ORIGIN

Query Match 25.2%; Score 370.4; DB 12; Length 991;
Best Local Similarity 99.0%; Pred. No. 6e-74;
Matches 384; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

674 CAGGACTTTTCTGACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 733
541 CAGGACTTTTCTGACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 482
734 GTGAATGACTTGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
481 GTGAATGACTTGTCT 422
794 CAGGACTTTTCTGACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 853
421 CAGGACTTTTCTGACACACACCTTGGCAACCTTCAGCCAGACGACGAGTCC 362
854 GAGGAGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 913
361 GAGGAGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
914 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 973
301 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245
974 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
244 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
1034 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 1061
184 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 157

RESULT 6
A0610898/c 476 bp DNA linear GSS 15-JUN-1999
LOCUS A0610898
DEFINITION HS 5105 A2 G06 SP6E RPCT-11 Human Male BAC Library Homo sapiens genomic clone Plate=681 Col=12 Row=M, genomic survey sequence.
ACCESSION A0610898
VERSION A0610898.1 GI:5072174
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Oy 245 TCGATGTTCTATGATGTCGCTGAAGAAACAGACCTGTGACACAGAGTTCAGAGGAGCGG 304
 Db 243 TCGATGTTCTATGATGTCGCTGAAGAAACAGACCTGTGACACAGAGTTCAGAGGAGCGG 302
 Oy 305 TCGGACGGTTTCTCCCAAGTCCCAAGTCCCGTGGTGAATCCGAATACCTGGAT 360
 Db 303 TCGGACGGTTTCTCCCAAGTCCCAAGTCCCGTGGTGAATCCGAATACCTGGAT 358
 RESULT 8
 B0894374 964 bp mRNA linear EST 16-AUG-2002
 LOCUS B0894374
 DEFINITION AGENCOURT_8623992 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6304287
 5', mRNA sequence.
 VERSION B0894374
 KEYWORDS B0894374.1 GI:22286388
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 964)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strauberg, Ph.D.
 Email: cga@b-remail.nih.gov
 Tissue Procurement: Lou Staude
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLND at:
 http://image.llnl.gov
 Plate: L10CM2524 row: 1 column: 16
 High quality sequence scope: 510.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="6304287"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7, site 1: XhoI; site 2:
 EcoRI; cDNA made by oligo-dT priming, directional cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCGACGAG(C). Size-selected 500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH-MGC
 library."
 BASE COUNT 196 a 277 c 268 g 223 t
 ORIGIN
 Query Match 23.7% Score 348.4; DB 13; Length 964;
 Best Local Similarity 98.5%; Pred. No. 6,2e-69;
 Matches 384; Conservative 1; Indels 5; Gaps 3;

Oy 852 AAGAGAGAGATGATGAGAGACACAGAGTGGCGTTCAGAGCCCTACATTGAC 911
 Db 377 AAGAGAGAGATGATGAGAGACACAGAGTGGCGTTCAGAGCCCTACATTGAC 918
 Oy 912 CACCTTCTTCTCTGAGGACAGAGACCAAGGCTCCAGGAGCTTCGAGAGCC 971
 Db 317 CACCTTCTTCTCTGAGGACAGAGACCAAGGCTCCAGGAGCTTCGAGAGCC 961
 Oy 972 TGAAGTCAAGAGAGCCCAAGGAGCTCTGATCCCAAGGAGCTCTGATCCGATT 1031
 Db 260 TGAAGTCAAGAGAGCCCAAGGAGCTCTGATCCCAAGGAGCTCTGATCCGATT 201
 Oy 1032 CTTGACGACAGAGCTGGGCGACACTGTGG 1061
 Db 200 CTTGACGACAGAGCTGGGCGACACTGTGG 171
 RESULT 9
 B7729118 640 bp mRNA linear EST 17-DEC-2002
 LOCUS B7729118
 DEFINITION B7729118 RIKEN full-length enriched, 7 days embryo whole body Mus
 musculus cDNA clone C430033A03 5', mRNA sequence.
 VERSION B7729118
 KEYWORDS B7729118.1 GI:27142245
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 640)
 AUTHORS Okazaki, Y., Putnam, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, B.,
 Mikado, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
 Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C.,
 Gojobori, T., Balderelli, R., Hill, D. P., Bulc, C., Hume, D. A.,
 Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
 Beisel, K. W., Blake, J. A., Brad, D., Bryant, C., Chochia, C., Corbett,
 L. E., Cousins, S., Daille, E., Dragani, T. A., Fletcher, C. F., Forrest,
 A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Glast, C., Godzik, A.,
 Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J. J.,
 Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R. M.,
 King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
 P. A., Maglott, D. R., Maltara, L., Marchionni, L., McKenzie, L., Miki,
 H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,
 Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
 Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,
 B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,
 M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
 R. D., Tomita, M., Verrado, R., Wagner, L., Wahlestedt, C., Wang, Y.,
 Watanabe, Y., Wells, C., Wilm, L. G., Wrynshaw-Borle, A., Yangisawa,
 M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A.,
 Carninci, P., Hayashizumi, N., Hirozane-Koshikawa, T., Kono, H., Nakamura,
 M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
 Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
 K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
 E. S., Rogers, J., Birney, E., and Hayashizumi, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 TITLE JOURNAL MEDLINE
 PUBMED 22354683
 1246851
 COMMENT Contact: Yoshihide Hayashizumi,
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saitama-cho, Tsukuba, Ibaraki, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Aikawa, T., Carninci, P., Fukuda,
 S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F., Imotani, K.,

Db 473 CTTCTCCAAA--GAACTGCCAGAGGGGTGTCAGCCCTCAAGTCAAGGCTCCGAC 416
 QY 811 CACCCACAGACAGATGAGAGAGACCTTGACAGAGAGAGAGAGAGAGATGAGAG 870
 Db 415 CACACACAGAGAGATGAGAGAGAGCTCTTGACAGAGAGAGAGAGAGATGAGAG 356
 QY 872 GAGACAGAGAGATGAGAGAGCTTGACAGAGAGAGAGAGAGAGATGAGAGAG 930
 Db 355 GTCACAGAGAGATGAGAGAGCTTGACAGAGAGAGAGAGAGAGATGAGAGAG 296
 QY 931 AGAGACAGAGAGCTTGACAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAG 990
 Db 295 AGAGACAGAGAGCTTGACAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAG 239
 QY 991 GGTCTCTGATCCAGAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
 Db 238 GGTCTCTGATCCAGAGAGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
 QY 1051 CAGCATGATGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
 Db 178 CAGCATGATGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
 QY 1111 GCCAG 1156
 Db 118 AGCAG 73

RESULT 11
 A0634533 558 bp DNA linear GSS 17-JUN-1999
 LOCUS RPCI-11-478C4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-478C4,
 DEFINITION genomic survey sequence.
 A0634533
 A0634533.1 GI:5097166
 GSS.
 KEYWORDS
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 558)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 J.C.

REFERENCE
 AUTHORS Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished
 CONTACT: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jg.med.buffalo.edu). Clones may be purchased from
 BACRAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@regen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: 17
 Classes: BAC ends.

FEATURES
 source
 1..558
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:768319"
 /db_xref="taxon:9606"
 /clone="RPCI-11-478C4"
 /sex="Male"
 /cell_type="lymphocytes"
 /clone_id="RPCI-11"
 /note="Vector: pBac3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 113 a 156 c 180 g 109 t
 ORIGIN
 Query Match 19.8%; Score 292; DB 28; Length 558;
 Best Local Similarity 100.0%; P-Id. No. 3.8e-56;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1181 GGTTCCTGAGAGAGCTTCCAGAGATACCTCTCTCTGAGAGAGAGAGAG 1240
 Db 1 GGTTCCTGAGAGAGCTTCCAGAGATACCTCTCTCTGAGAGAGAGAGAGAG 60
 QY 1241 CCAACCGAG 1300
 Db 61 CCAACCGAG 120
 QY 1301 TGTCTGAG 1360
 Db 121 TGTCTGAG 180
 QY 1361 GATCGGAG 1420
 Db 181 GATCGGAG 240
 QY 1421 GGGCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1472
 Db 241 GGGCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 292

RESULT 12
 B1104593 620 bp mRNA linear EST 26-JUN-2001
 LOCUS B1104593
 DEFINITION mRNA sequence.
 B1104593
 B1104593.1 GI:14555486
 EST.
 KEYWORDS
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 620)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plate: LLM1101 row: c column: 10
 High quality sequence start: 5
 High quality sequence stop: 556
 Location/Qualifiers
 1..620
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CEB111"
 /db_xref="taxon:10090"
 /clone="IMAGE:5036481"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /clone_id="NCI CGAP Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

FEATURES

source

BASE COUNT 140 a 186 c 168 g 126 t
 ORIGIN

| Query Match Similarity | 16.1%; | Score 237.4; | DB 12; | Length 620; |
|------------------------|-----------------|--|------------|-------------|
| Best Local Similarity | 71.5%; | Pred. No. 1,1e-43; | | |
| Matches 338; | Conservative 0; | Mismatches 146; | Indels 13; | Gaps 6 |
| Qy | 7 | ATGCGGGGCCCGAGCGCTGGAGGCCCTCTGCTCTG--TGCCTGCTGAG--GCCTCTGAG | 64 | |
| Db | 16 | ATGTGGCCGGGCGAGACCGGTGTGGGCCCTTACTCTGTGTTCTGTGTCAGAGACCCCTGAG | 75 | |
| Qy | 65 | GGAGGCCCGCCGCTGGAGCCCCCTCCCGAAGATGTGACGCTGCTGCCAGAACTTTCAGCGGT | 124 | |
| Db | 76 | GAAAGCCCCCGCTAGGCCCCCAACCAAGAGACCTCTTCTCCAGAACTTCACTGT | 135 | |
| Qy | 125 | ACCTGACATGCGCTCCCGAGGCTTGGCAACCCCGAGATGTGACTTATTTTGTGGCTATC | 184 | |
| Db | 136 | ACCTACCAATGCGCTTCCGGGGCTTGGGAGCCCCCGAATGTGACTTATTTCTGTGACTAC | 195 | |
| Qy | 185 | AGAGCTCTCCACCCCGTAGACGGTGGCGAGAGTGGAGAGTGTGGCGGAAACCAAGAGC | 244 | |
| Db | 196 | AAGAGTAT---ATCAAAACCGGTGTGGCAACAGATGAGACATTTGTGAGTATCAAGCTC | 252 | |
| Qy | 245 | TGCTATGTTCTATGATGTGCTGAGAAAGAAACGAGACTGTACA--ACAAGTTACGGAGCG | 303 | |
| Db | 253 | TGCTATGTGCCCCCTGATATGTGCTGAGAAACGTGAACCTGTACATCCAAAGTTACAAAGGACA | 312 | |
| Qy | 304 | GTGCGAGCGGTTTCTCCAGACTCAAGTCCCCCTGGGTGAGTCCGAATACCTGAGATTAC | 363 | |
| Db | 313 | GTACAGGCAAGCTTCCGACAGGGCAGGTCTCCACGGGTGAGTCCCGGATCTGTGAATAC | 372 | |
| Qy | 364 | CTTTTGAAGTGAAGCCGCGCCCACTGTCTGTGTGTGACCCGACGAGAGAAATCTTG | 423 | |
| Db | 373 | CTTTTGAAGTGAAGCTGAGCCCGACCACTGTGTGTGACCCGACGAGAGAAATCTTA | 432 | |
| Qy | 424 | AGTGCAAATGCAGATACAGCTGCCCCCTGCATGCCCCCACTGAGATCTGAAATATGAG | 483 | |
| Db | 433 | AGGGTCA--TGCTACTACAGATGCAACCTTGCATGCGGTGGAAGTAAATACAG | 490 | |
| Qy | 484 | GTGGCAATCTGAGAGAGGGGGCCGGAACAGAG-----CCGATTTTCATGCACTCCCC | 538 | |
| Db | 491 | GTGGCAGTTTGTGACAGAGAGGCTGTGGAGAAAGCAAGACCCATATCTCTTCACTCTCT | 550 | |
| Qy | 539 | ATGCGCACCGCACTGTCAG | 555 | |
| Db | 551 | ATGCGCACCGCACTGTCAG | 567 | |

```

RESULT 13
CB713061
LOCUS
DEFINITION CB713061 496 bp mRNA linear EST 10-APR-2007
AMERICAN:RHVS-00223-G11.4 W Rat hypothalamus (10471) Rat
nervogenic cDNA clone rhvs-00223-g11.5', mRNA sequence.
ACCESSION .CB713061
VERSION .CB713061
KEYWORDS CB713061.1 GI:29770209
SOURCE EST.
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 496)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00223 row: 9 column: 11.
Location/Qualifiers
1. 496
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
FEATURES
SOURCE

```

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|---------------------------|--|--|
| | /clone="rhny5"-00223-911" | |
| | /clone_1fb="W Rat hypochthalmus (10471)" | |
| | /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; W Rat | |
| | hypochthalmus adult female M18cat rat avg. Insert Size 2.3 | |
| | Kb fraction 6 and 7" | |
| BASE COUNT | 109 a 155 c 135 g 97 t | |
| ORIGIN | | |
| .Query Match | 15.2%; Score 223.8; DB 14; Length 496; | |
| Best Local Similarity | 72.4%; Pred. No. 1.3e+00; | |
| Matches 331; Conservative | 0; Mismatches 97; Indels 29; Gaps 2 | |
| Oy | 7 ATGGCGGCGGCCGAGGCGCTGGSGCCCTCTCTCTGTGGCTGTGCACAGCCGCTCCAAGG 66 | |
| Dd | 55 ATGCGGCGGCGCTGGCGCGGCGGCGCCCTTACTCTCTGTTCCTGAAGCAAAAGCGCCCTAGA 114 | |
| Oy | 67 AGGCGCGCGCTGTGCCCCCTCCCGAATGTGACGCGCTCTCCCAAGAACCTTCACGCGTGAC 126 | |
| Dd | 115 AGGCGCGCGCTGTAGCACCACCCAGAAAGTGTAACACTGCTCTCCAGAAATTTCACGTTTAC 174 | |
| Oy | 127 CTGACATAGGCTCCGAGGCGTTGGGACACCCCGAGAAATGTACATATTGTGGCTATACAG 186 | |
| Dd | 175 CTGACATAGGCTCCGAGGCGTGGGTAGCGCCCGAGAAATGTACATCTTGTGACCTTACAA 234 | |
| Oy | 187 AGCTCTCCACCCGTAAGACGCGTGGCGGAAGTGAAGATGTGGCGGAAACCAAGAGCTG 246 | |
| Dd | 235 AGCTATAACATCAT-----TGGCGAAAGTAGAGCATGTGGCGGCACTACATCTCTG 288 | |
| Oy | 247 CTATGTTCTATATGTGCGCTGGAAGAAACAGACCTGTACCAACAAGTTCAAGGGAGCGG 306 | |
| Dd | 289 GTGTGTCTCCATATATGTGCTGTGAAGAAACAGACCTGTACATCAAGTTCAAAGTCAAGTA 348 | |
| Oy | 307 CGGACGGTTCTCCAGCTCCAGTCCCCTCTGGGTGGAAGTCCGAATACCTGATTAATT 366 | |
| Dd | 349 CAGGCACTTCTCCCATATGTAGATGTCCCAATGGGTGAGATCC----- 390 | |
| Oy | 367 TTTGAATGGAGCGGCGCCCACTGTCTGTGCTCAACCAAGACGAGAGATCTGACT 426 | |
| Dd | 391 -----AGTGAAGTAGCCCAACCAACCTGTGTCTCTCCAGAAAGGAAGATCTTAAT 445 | |
| Oy | 427 GCCAATGCCATACAGAGTCCCCCTCTGATGATCCC 463 | |
| Dd | 446 GTCAAGCTATCAACAGGTGCAACCTGTGATGCTTC 482 | |

RESULT 14
LOCUS B1657668
DEFINITION Mus musculus CDNA clone IMAGE:5325386 5',
ACCESSION B1657668
VERSION B1657668
KEYWORDS GI:15571904
SOURCE EST.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 609)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lochar Hamminghausen Ph.D., Princeton Puth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1826 row: a column: 11
High quality sequence stop: 609.

FEATURES
source

Location/Qualifiers
1. 609
/organism="Mus musculus"
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/strain="NMRI"
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/clone="IMAGE:532586"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam4"
/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Firth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

BASE COUNT 145 a 176 c 162 g 126 t

ORIGIN

Query Match 13.2%; Score 193.8; DB 12; Length 609;
Best Local Similarity 71.0%; Pred. No. 1e-33;
Matches 284; Conservative 0; Mismatches 110; Indels 6; Gaps 2;

674 CAGACCTTTCGACACACACACCTTGGCACTTTACGCCGACGACACAGTCC 733
189 CAGACCTTTCGACACACACACCTTGGCACTTTACGCCGACGACACAGTCC 248
734 GTGATGACTTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 793
249 TCTGATGACTTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 308
794 CGAGTCAGGGGCCCCAGCCCAAGACAGACAGAGAGAGAGAGAGAGAGAG 853
309 CAGGTCAAGAACCCAGCCAGCTTACAGGACAGACAGACAGACAGACAG 368
854 GAGGAGAGAGATGAGAGACACAGACAGAGAGAGAGAGAGAGAGAGAG 913
369 GACGAGAGACACAGACACAGACAGAGAGAGAGAGAGAGAGAGAGAG 425
914 CCTTCTTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 970
426 CCCCCTTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 485
971 GTGACTCAG 1030
486 GTGATTCAG 545
1031 TCTTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
546 TCTTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585

RESULT 15
A0772013c 506 bp DNA linear GSS 29-JUL-1999
LOCUS HS_5413.B2.H01.SPEB.RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION A0772013 genomic clone Plate=989 Col=2 Row=P, genomic survey sequence.
ACCESSION A0772013.1 GI:5651741
VERSION GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 506)
Mahafras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589

PUBMED 10449764
CONTACT: Mahafras G.G., Wallace J.C., Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEL: (206) 616-3618
FAX: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htrc.washington.edu
Plate: 989 row: P column: 2
Seq primer: SP6
Clase: BAC ends
High quality sequence stop: 506.

FEATURES
source

Location/Qualifiers
1. 506
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=989 Col=2 Row=P"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 111 a 153 c 97 g 144 t 1 others

ORIGIN

Query Match 12.8%; Score 188.2; DB 28; Length 506;
Best Local Similarity 80.1%; Pred. No. 1.8e-32;
Matches 258; Conservative 0; Mismatches 59; Indels 5; Gaps 3;

839 CTTCAGAGACGAAAGAGAGAGAGATGAGAGAGACACAGAAATGCGTACCTTCAG 898
322 CTTCAGATGACAAAGAGATGAGATGAGAGAGAGACACATGATGATTAATACCA 264
899 CCTTATATTGAACCACTCTTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 958
263 CCTTATATTGAACCTCTCTTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 205
959 GCCTTGT 1018
204 TCCTTGT 148
1019 TCTGT 1078
147 TCTGT 88
1079 GTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1138
87 GTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 28
1139 CACCAAGATCTCTCCACAC 1160
27 CACCAAGATCTACACCTCCAC 6

Search completed: September 17, 2003, 22:13:27
Job time : 2189.19 secs